

SEQUENCE LISTING



<110> AMRAD Operations Pty Ltd

<120> A NOVEL MAMMALIAN GENE, bcl-2, BELONGS TO THE bcl-2
FAMILY OF APOPTOSIS-CONTROLLING GENES

<130> 2096584

<140> 09/155,327

<141> 1997-03-27

<150> FN8965

<151> 1996-03-27

<160> 12

<170> PatentIn Ver. 2.1

<210> 1

<211> 33

<212> DNA

<213> Mouse

<400> 1

gctctagaac tggggahgir tigtigcctt ytt

33

<210> 2

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<220>

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<222> 5

<223> Xaa is Ile or Val

<400> 2

Asn Trp Gly Arg Xaa Val Ala Phe Phe

1

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<212> DNA
<213> Mouse

<400> 3
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31

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<400> 4
Trp Ile Gln Xaa Xaa Gly Gly Trp
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<210> 5
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<400> 5
Met Ala Thr Pro Ala Ser Thr Pro Asp Thr Arg Ala Leu Val
1 5 10

<210> 6

<211> 583
<212> DNA
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<220>
<221> CDS
<222> (1)..(579)

<400> 6

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Phe Val Gly Tyr Lys Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly

20 25 30

ccc ggg gag ggc cca gca gct gac ccg ctg cac caa gcc atg cgg gca 144
Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala

35 40 45

gct gga gat gag ttc gag acc cgc ttc cgg cgc acc ttc tct gat ctg 192
Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu

50 55 60

gcg gct cag ctg cat gtg acc cca ggc tca gcc cag caa cgc ttc acc 240
Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr

65 70 75 80

cag gtc tcc gac gaa ctt ttt caa ggg ggc ccc aac tgg ggc cgc ctt 288
Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu

85 90 95

gta gcc ttc ttt ctc ttt ggg gct gca ctg tgt gct gag agt gtc aac 336
Val Ala Phe Phe Leu Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn

100 105 110

aag gag atg gaa cca ctg gtg gga caa gtg cag gag tgg atg gtg gcc 384
Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Glu Trp Met Val Ala

115 120 125

tac ctg gag acg ~~ctg~~ ctg gtc gac tgg atc cac agc ~~agg~~ ggg ggc tgg 432
 Tyr Leu Glu Thr Arg Leu Val Asp Trp Ile His Ser Ser Gly Gly Trp
 130 135 140

gcg gag ttc aca gct cta tac ggg gac ggg gcc ctg gag gag gcg cgg 480
 Ala Glu Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Glu Ala Arg
 145 150 155 160

cgt ctg cgg gag ggg aac tgg gca tca gtg agg aca gtg ctg ~~acg~~ ggg 528
 Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Arg Thr Val Leu Thr Gly
 165 170 175

gcc gtg gca ctg ggg gcc ctg gta act gta ggg gcc ~~ttt~~ ttt gct agc 576
 Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser
 180 185 190

aag tgaa 583
 Lys

<210> 7
 <211> 193
 <212> PRT
 <213> HUMAN

<400> 7
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Phe Val Gly Tyr Lys Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly
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Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala
 35 40 45

Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu
 50 55 60

Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr
 65 70 75 80

Gln Val Ser Asp Leu Phe Gln Gly Gly Pro Asn Thr Gly Arg Leu

85

90

95

Val Ala Phe Phe Leu Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn

100

105

110

Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Glu Trp Met Val Ala

115

120

125

Tyr Leu Glu Thr Arg Leu Val Asp Trp Ile His Ser Ser Gly Gly Trp

130

135

140

Ala Glu Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Glu Ala Arg

145

150

155

160

Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Arg Thr Val Leu Thr Gly

165

170

175

Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser

180

185

190

Lys

<210> 8

<211> 581

<212> DNA

<213> Mouse

<220>

<221> CDS

<222> (1)..(579)

<400> 8

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Met Pro Thr Pro Ala Ser Thr Pro Asp Thr Arg Ala Leu Val Ala Asp

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15

ttt gta ggc tat agg ctg agg cag aag ggt tat gtc tgt gga gct ggg 96

Phe Val Gly Tyr Arg Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly

cct ggg gaa ggc cca gcc gcc gac ccg ctg cac caa gcc atg cgg gct 144
 Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala
 35 40 45

gct gga gac gag ttt gag acc cgt ttc cgc cgc acc ttc tct gac ctg 192
 Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu
 50 55 60

gct gct cag cta cac gtg acc cca ggc tca gcc cag caa cgc ttc acc 240
 Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr
 65 70 75 80

cag gtt tcc gac gaa ctt ttc caa ggg ggc cct aac tgg ggc cgt ctt 288
 Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu
 85 90 95

gtg gca ttc ttt gtc ttt ggg gct gcc ctg tgt gct gag agt gtc aac 336
 Val Ala Phe Phe Val Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn
 100 105 110

aaa gaa atg gag cct ttg gtg gga caa gtc cag gat tgg atc gtg gcc 384
 Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Asp Trp Ile Val Ala
 115 120 125

tac ctg gag aca cgt ctg gct gac tgg atc cac agc agt ggc ggc tgg 432
 Tyr Leu Glu Thr Arg Leu Ala Asp Trp Ile His Ser Ser Gly Gly Trp
 130 135 140

gcg gac ttc aca gct cta tac ggg gac ggg gcc ctg gag gac gca cgg 480
 Ala Asp Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Asp Ala Arg
 145 150 155 160

cgt ctg cgg gag ggc aac tgg gca tga gtg agc aca gtg gtg acg ggg 528
 Arg Leu Arg Glu Gly Asn Trp Ala Val Ser Thr Val Val Thr Gly Ala
 165 170 175

gcc gtg gca ctg ggg gcc ctg gta act gta ggg gcc ttt ttt gct agc 576
 Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser Lys
 180 185 190

<210> 9

<211> 192

<212> PRT

<213> Mouse

<400> 9

Met Pro Thr Pro Ala Ser Thr Pro Asp Thr Arg Ala Leu Val Ala Asp
 1 5 10 15
 Phe Val Gly Tyr Arg Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly
 20 25 30
 Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala
 35 40 45
 Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu
 50 55 60
 Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr
 65 70 75 80
 Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu
 85 90 95
 Val Ala Phe Phe Val Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn
 100 105 110
 Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Asp Trp Ile Val Ala
 115 120 125
 Tyr Leu Glu Thr Arg Leu Ala Asp Trp Ile His Ser Ser Gly Gly Trp
 130 135 140
 Ala Asp Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Asp Ala Arg
 145 150 155 160
 Arg Leu Arg Glu Gly Asn Trp Ala Val Ser Thr Val Val Thr Gly
 165 170 175
 Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser
 180 185 190
 Lys